



# New strategies for the determination of cyanotoxins using high resolution mass spectrometry

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# Cyanobacteria

- **Cyanobacteria**, or blue-green algae, appear naturally, in most cases without toxicity.
- **Intense proliferation** is linked to both human and animal intoxication cases.
- The production of toxic metabolites is the main cause → **cyanotoxins**.
- The production of cyanobacteria, as well as their cyanotoxins, is almost **impossible to predict** precisely.
- Annual cost of harmful blooms > \$ 800M in the US



Reporting contaminated water bodies.



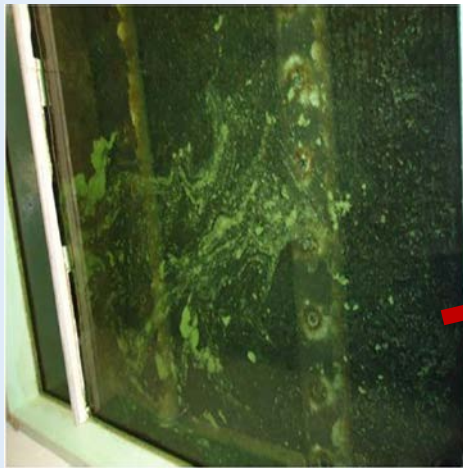


# Widespread algal blooms on Lake Erie

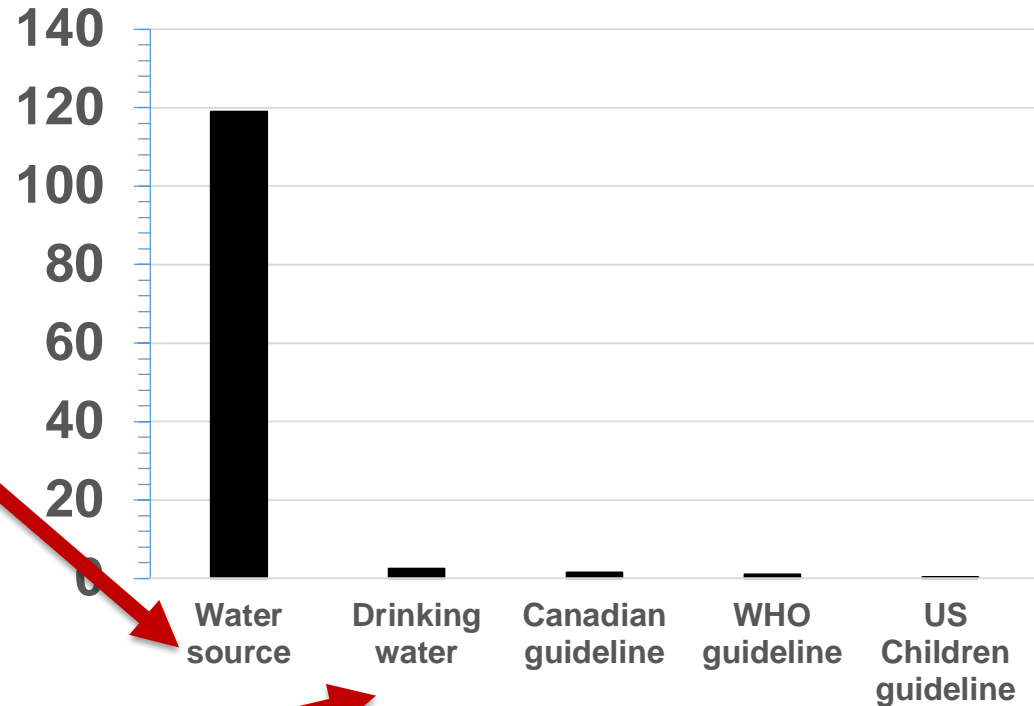


- The growth of blue-green algae is a function of heat and nutrients.
- Agricultural wastes and climate change aggravate the situation.

# Drinking water treatment plant



Toxin concentration ( $\mu\text{g MC/L}$ )



- River water 119  $\mu\text{g MC/L}$
- Drinking water 2,5  $\mu\text{g MC/L}$
- Children protection guideline 0.3  $\mu\text{g MC/L}$  (USEPA June 2015)

# Problematics

- Cyanotoxins are considered as an emerging threat in aquatic environments but also in water supply systems.
- The development of future analytical methods for cyanotoxins faces many challenges.
- The diversity of toxins and congeners, with different physicochemical properties makes it difficult, to date, the ability to detect and quantify the majority of cyanobacterial toxins.
  - various degradation conditions
  - different conditions of storage
  - different extraction / analysis conditions
  - distribution and availability of standards
  - Analytical costs



# Determination of $\beta$ -*N*-methylamino-L-alanine

- The non-proteinogenic amino acid  $\beta$ -*N*-methylamino-L-alanine (**BMAA**) is an excitotoxic neurotoxin.
- BMAA is possibly related to amyotrophic lateral sclerosis/Parkinson's disease complex (ALS/PDC).
- More than **95 % of toxic cyanobacterial** can produce BMAA, suggesting its presence in aquatic environments.
- No regulation and no monitoring are in place in North America.



*Cycas circinalis*



*Cycas circinalis* seeds

# Previous work

Several analytical methods have been published for the detection of BMAA, but **few consensuses** have been made on the reported concentrations.

## HPLC-FD

- Derivatization with 6-ACQ
- Overestimation → derivatization of other amino acids and small molecules

## HPLC-MS & MS/MS

- Derivatization with 6-ACQ for improved selectivity

## HILIC-MS/MS

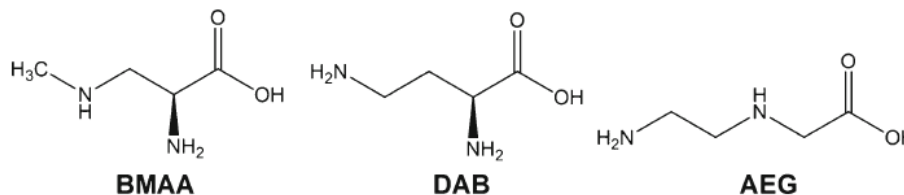
- Simplified method
- High dependency on the chromatographic separation

Few methods which include BMAA to other cyanotoxins in a single analysis

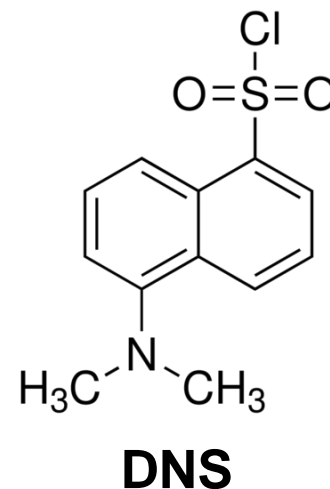
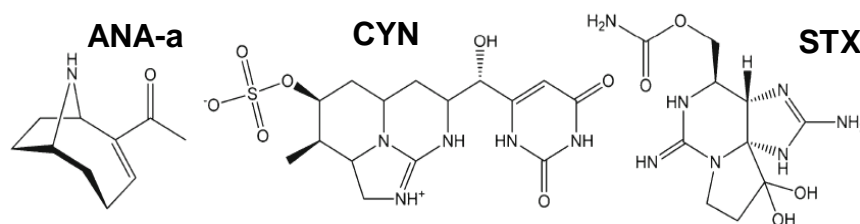
# Objectives

The aim of this work is to:

- develop an analytical method for the detection of **BMAA** and two isomers, **DAB** and **AEG**, using **dansyl chloride (DNS)** derivatization.



- include three alkaloid cyanotoxins: **anatoxin-a**, **cylindrospermopsin** and **saxitoxin**.



- use UHPLC-HESI-HRMS in a fragmentation mode to determine the fragmentation patterns and then suggest their **fragment structures** using Mass Frontier™ 7.0 software.
- apply the method to real field-collected cyanobacterial bloom water samples.



# Workflow

100 mL lake water

Cell lysis  
Freeze/thaw x 3

Internal standard addition

Filtration  
Nitrocellulose 0.22 µm

pH to 4 with citric acid

**Solid Phase extraction**

Cation exchange SPE 200 mg

**Conditioning**

5 mL MeOH/5 mL H<sub>2</sub>O pH 4

**Wash**

5 mL H<sub>2</sub>O pH 4 MeOH (90:10 v/v)

**Elution**

5 mL MeOH with 3% NH<sub>4</sub>OH

**Nitrogen drying at 35°C**

**Reconstitution step**

250 µL Borax buffer (0.2 M) + 250 µL  
DNS (1 mg mL<sup>-1</sup> in acetone)

**Derivatization**

60°C, 10 minutes

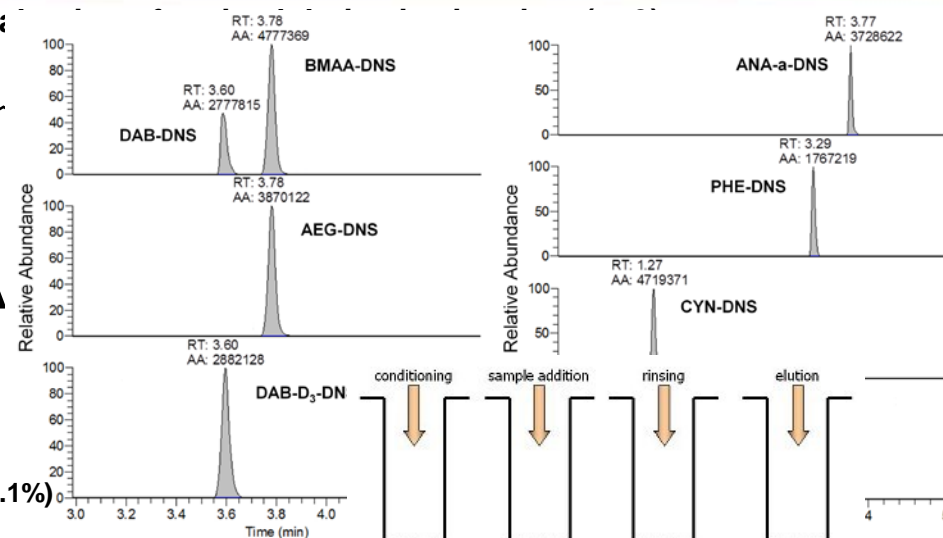
**UHPLC-HESI-MS analysis**

## Chromatographic conditions

### Eluent gradients

Time (min)	A (%)	B (%)
0.00	70	30
2.00	10	90
4.00	0	100
6.00	0	100
6.01	70	30
10.00	70	30

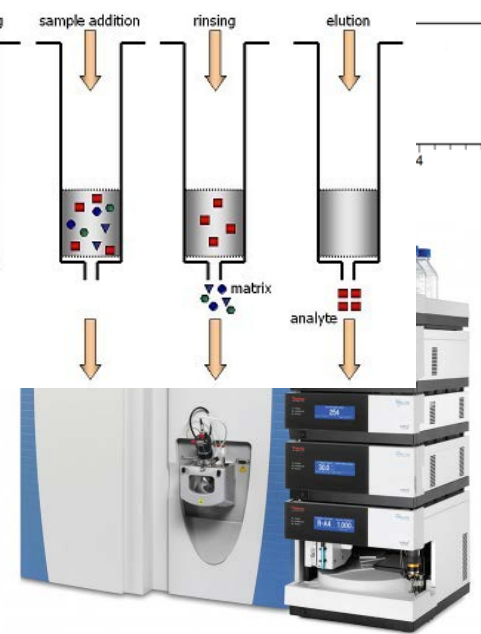
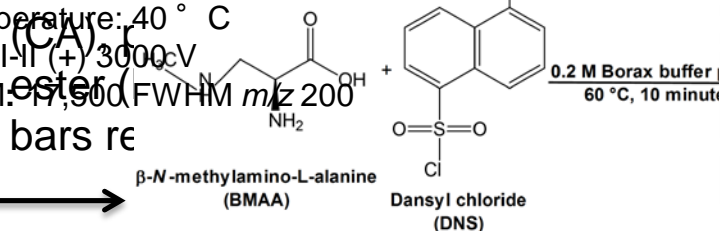
A: Water + formic acid (0.1%)  
B: Acetonitrile + formic acid (0.1%)



Thermo Scientific Dionex Ultimate™ 3000 UHPLC.  
Q Exactive™ Hybrid Quadrupole-Orbitrap, Thermo Scientific.

Time (min)

- Hypersil GOLD C18 (100 mm, 2,1 mm, 1,9 µm)
- Injection: 25 µL
- Flow: 0.2 mL min<sup>-1</sup>
- Temperature: 40 °C
- HESI-III (+) 3000 V
- PRM: 11,500 FWHM m/z 200



**Q Exactive mass spectrometer**

Roy-Lachapelle, A. et al., *Analytical Bioanalytical Chemistry*, 2015, **407**(18): p. 5487-5501.

<http://www.nationalanalyticalcorp.com/>

<http://www.thermoscientific.com/en/product/q-exactive-hybrid-quadrupole-orbitrap-mass-spectrometer.html>

# Fragment identification

## Mass Frontier™ 7.0 software

The screenshot displays the HighChem Mass Frontier 7.0 software interface. The main window shows a chemical structure of a dimethylamino-terminated sulfonamide derivative. The structure is shown in two views: a full structure and a fragmented structure. The fragmented structure is labeled with  $m/z$  599.1993. The fragmentation mechanism is shown with arrows and labels:  $+H^+$  and  $rH_B$ . The resulting fragment is a dimethylamino-terminated sulfonamide derivative, labeled with  $m/z$  277.1005. The software interface includes a menu bar (File, Edit, View, Tools, Search, Library, Options, Help), a toolbar, and a sidebar with various tools (Structure Editor, Database Manager, Chromatogram Processor, Spectra Classifier, Fragments Comparator, Isotope Pattern, Periodic Table, Formula Generator, Fragments and Mechanisms, Batch Fragment Generation, Report Creator, Structure Table). The main window also displays a list of mass-to-charge ratios ( $m/z$ ) and a search bar for possible fragments with  $m/z$  277.1005. The bottom status bar shows the chemical formula  $C_{29}H_{34}N_4O_6S_2$ , the  $m/z$  598.19198, and the number of fragments: 418 total non-isobaric fragments and 72 unique  $m/z$ .

# Fragments

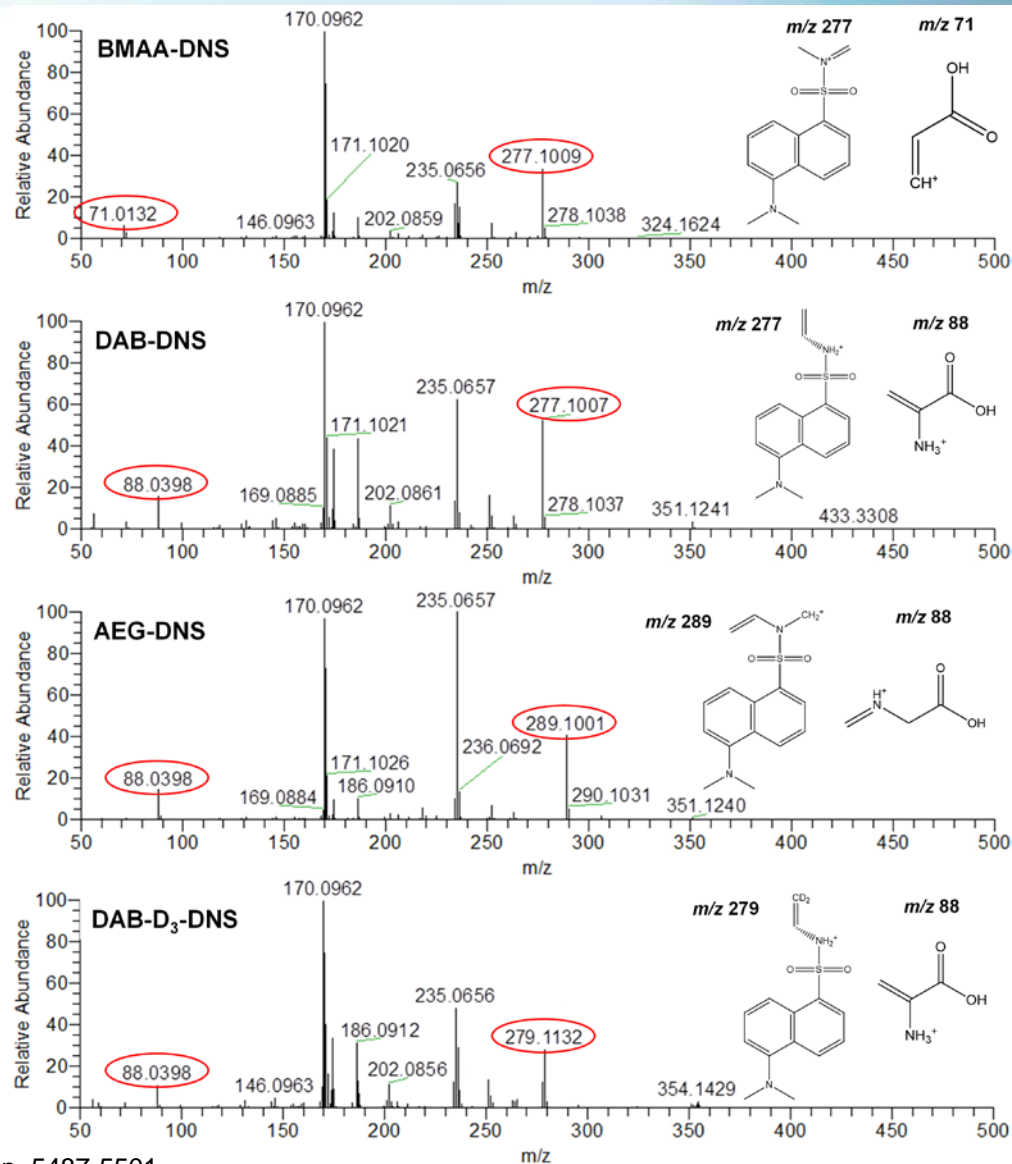
## Experimental precursor masses ( $m/z$ )

- BMAA, DAB and AEG: 585.1836
- ANA-a: 399.1737
- CYN: 649.1744
- SXT: 533.1925
- DAB-D<sub>3</sub>: 588.2024

Average mass accuracy < 2 ppm

## Due to BMAA and AEG coelution:

Unique fragments are used and their signal ratios are monitored to ensure no false positives are present.





# Results from bloom water samples

Cyanotoxins detection in lake samples ( $\mu\text{g L}^{-1}$ ) with relative standard deviation (RSD-%)

No. Sample	Location	BMAA	DAB	AEG	ANA-a	CYN	SXT
1	Lanaudière	ND	ND	ND	ND	ND	ND
2	Montérégie	ND	<b>0.01 (7)</b>	<b>0.08 (8)</b>	<b>0.1 (7)</b>	ND	ND
3	Montérégie	<b>0.2 (9)</b>	ND	ND	ND	ND	ND
4	Montérégie	ND	ND	<b>0.05 (10)</b>	ND	ND	ND
5	Etrie	ND	ND	ND	<b>0.08 (9)</b>	ND	ND
6	Etrie	<b>0.03 (8)</b>	<b>0.04 (8)</b>	<b>0.05 (9)</b>	<b>0.02 (7)</b>	ND	ND
7	Saguenay	ND	<b>0.009 (10)</b>	<b>0.06 (8)</b>	ND	ND	ND
8	Saguenay	<b>0.3 (10)</b>	<b>0.008 (11)</b>	<b>0.009 (11)</b>	ND	<b>0.2 (9)</b>	ND
9	Abitibi-Témiscamingue	ND	ND	ND	<b>0.2 (6)</b>	ND	ND
10	Abitibi-Témiscamingue	<b>0.01 (8)</b>	ND	ND	ND	ND	ND
11	Abitibi-Témiscamingue	ND	<b>0.03 (9)</b>	ND	<b>0.03 (8)</b>	<b>0.1 (11)</b>	ND
12	Montérégie	ND	ND	<b>0.01 (5)</b>	<b>0.01 (6)</b>	ND	ND

**SPE recoveries:** 86 to 103 %

**Signal recoveries from matrix effects:** 75 to 96 %

**Method detection limits (MDL):** 0.008 to 0.01  $\mu\text{g L}^{-1}$

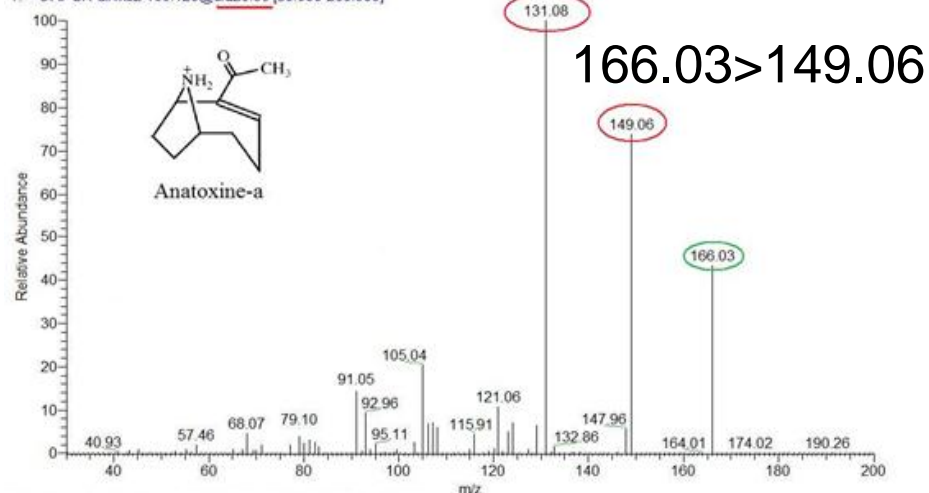
→ an order of magnitude lower than published methods



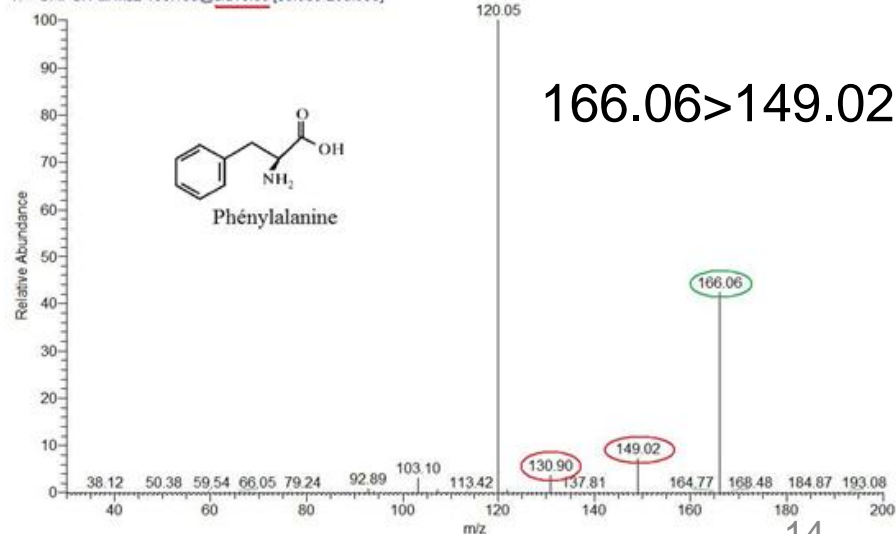
# Analytical challenges

- Spectroscopic detection methods are **avoided** due to the instability of ANA-a in contact with UV light.
- Most of the developed methods are based on **LC-MS/MS**.
- Phenylalanine, an essential amino acid, is an **isobaric interference** of ANA-a using MS/MS detection.
- Some similarities in terms on chromatographic separation, may lead to misidentification.

ANA 2 ppm full scan product Ce 20 #46 RT: 0.23 AV: 1 NL: 6.95E5  
T: + c APCI Full ms2 166.120@cid20.00 [30.000-200.000]



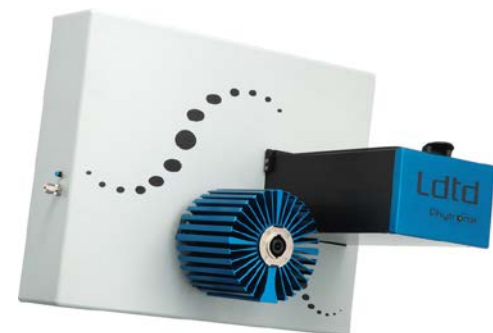
full scan product 2 ppm ce 10 #47 RT: 0.25 AV: 1 NL: 1.67E6  
T: + c APCI Full ms2 166.100@cid10.00 [30.000-200.000]





## Anatoxin-a analysis using LDTD-APCI-HRMS

- LDTD: Laser Diode Thermal Desorption (Phytronix Technologies)
- instant information of possible contamination
- simple, robust, lower costs, fast (< 10 sec / sample).
- A minimal resolution of **4,500 FWHM** is needed to resolve the mass signals of anatoxin-a and phenylalanine.
- Using PRM (Parallel Reaction monitoring) mode, a resolving power of **17,500 FWHM** ( $m/z$  200) with the Q Exactive

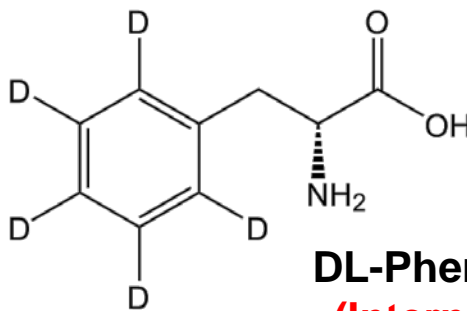
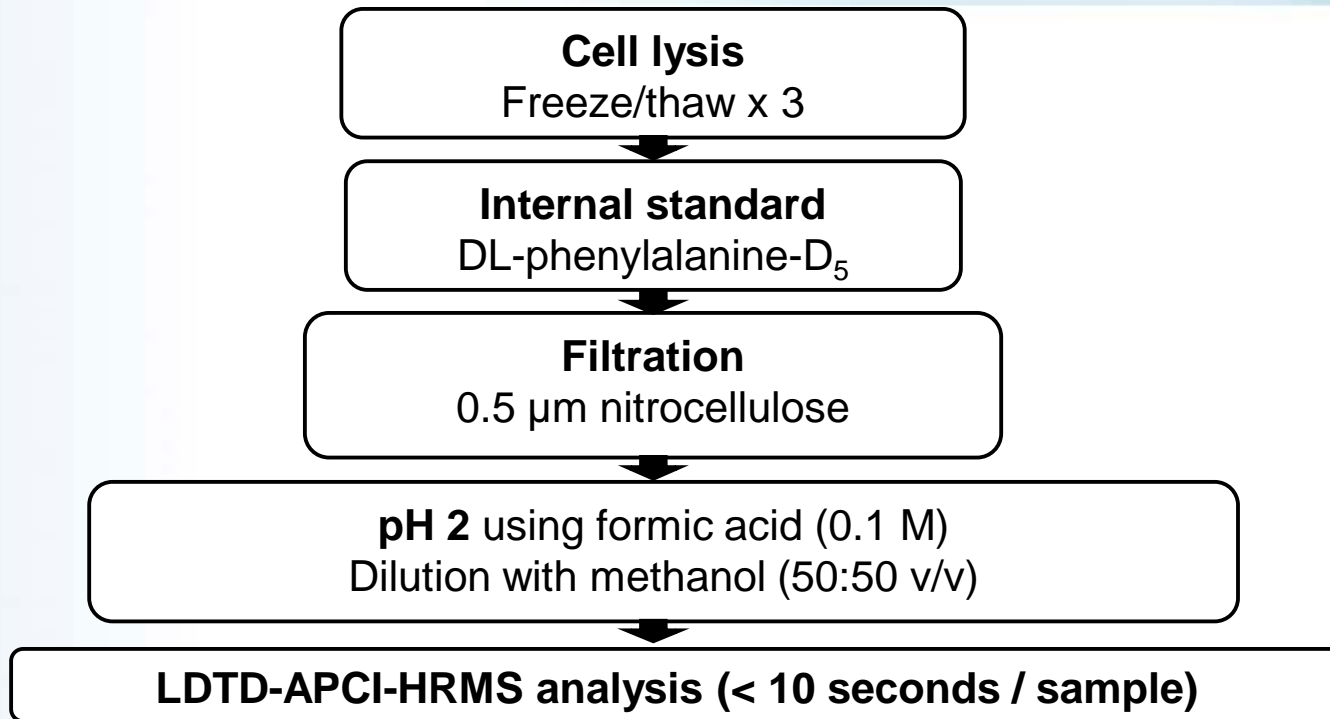


LDTD-APCI



Q Exactive

# Workflow



**DL-Phenylalanine-D<sub>5</sub>**  
**(Internal standard)**

# ANA-a and phenylalanine resolution

Mass error < 1 ppm

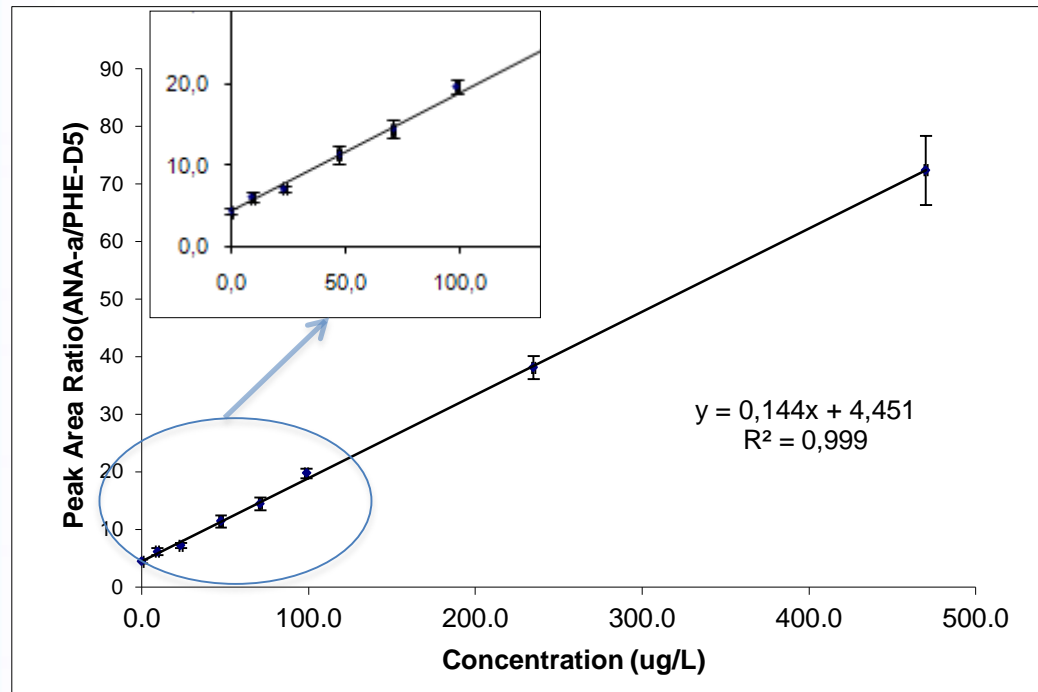
**Second most abundant  
isotopes**





# Analysis of ANA-a using the LDTD-APCI-HRMS

## Internal calibration by standard addition method (ANA-a/PHE-D5)



Calibration curve showing the linearity of the LDTD experiment

Method detection limit (MDL):  $0.2 \mu\text{g L}^{-1}$

Method quantification limit (MQL):  $0.6 \mu\text{g L}^{-1}$

Regulations:  $3.7 \mu\text{g L}^{-1}$  (Québec) and  $6.0 \mu\text{g L}^{-1}$  (New Zealand).

# Anatoxin-a detection in lake samples

Sample	Location	FS mode detection ( $\mu\text{g L}^{-1}$ )	PRM mode detection ( $\mu\text{g L}^{-1}$ )	LC-MS/MS* detection ( $\mu\text{g L}^{-1}$ )
1	Estrie	2.5 (11)	ND	0.1
2	Estrie	1.1 (9)	ND	0.02
3	Saguenay	ND	ND	0.01
4	Saguenay	ND	ND	0.01
5	Abitibi-Témiscamingue	1.9 (10)	0.21 (7)	0.2
6	Abitibi-Témiscamingue	ND	ND	0.01
7	Abitibi-Témiscamingue	1.6 (12)	ND	0.02
8	Montréal	ND	ND	0.01

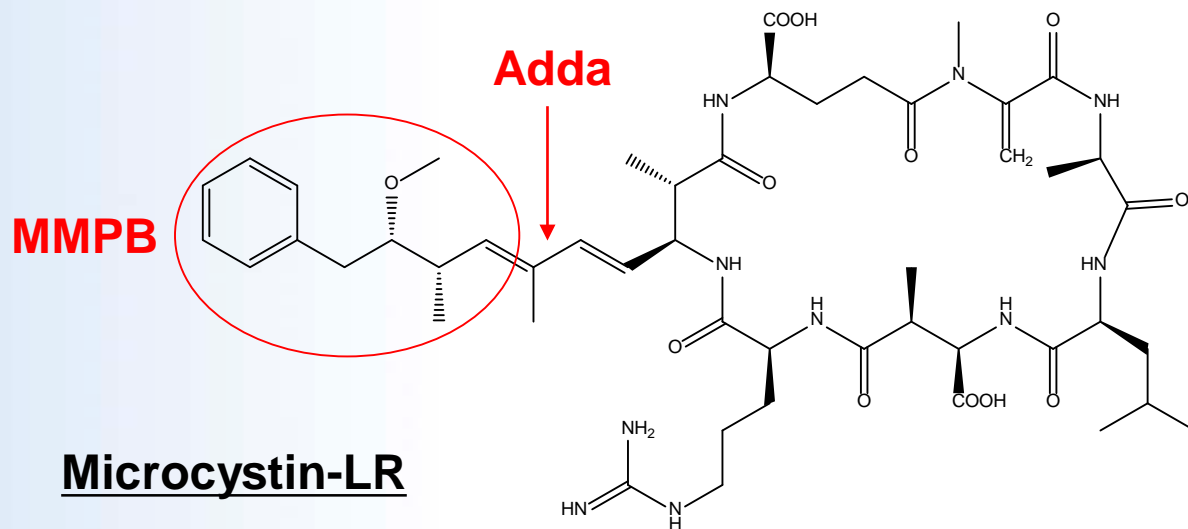
\* Quantified by the *Centre d'Expertise en Analyse Environnementale du Québec (CEAEQ)*, the analytical services of the *Ministère du Développement Durable, de l'Environnement et de la Lutte contre les Changements Climatiques (MDDELCC)*.

**Matrix effects (FS): 98 to 172 %**

**Matrix effects (PRM): 98 to 102 %**

# Determination of total microcystins in fish

## Microcystin structures (MC)



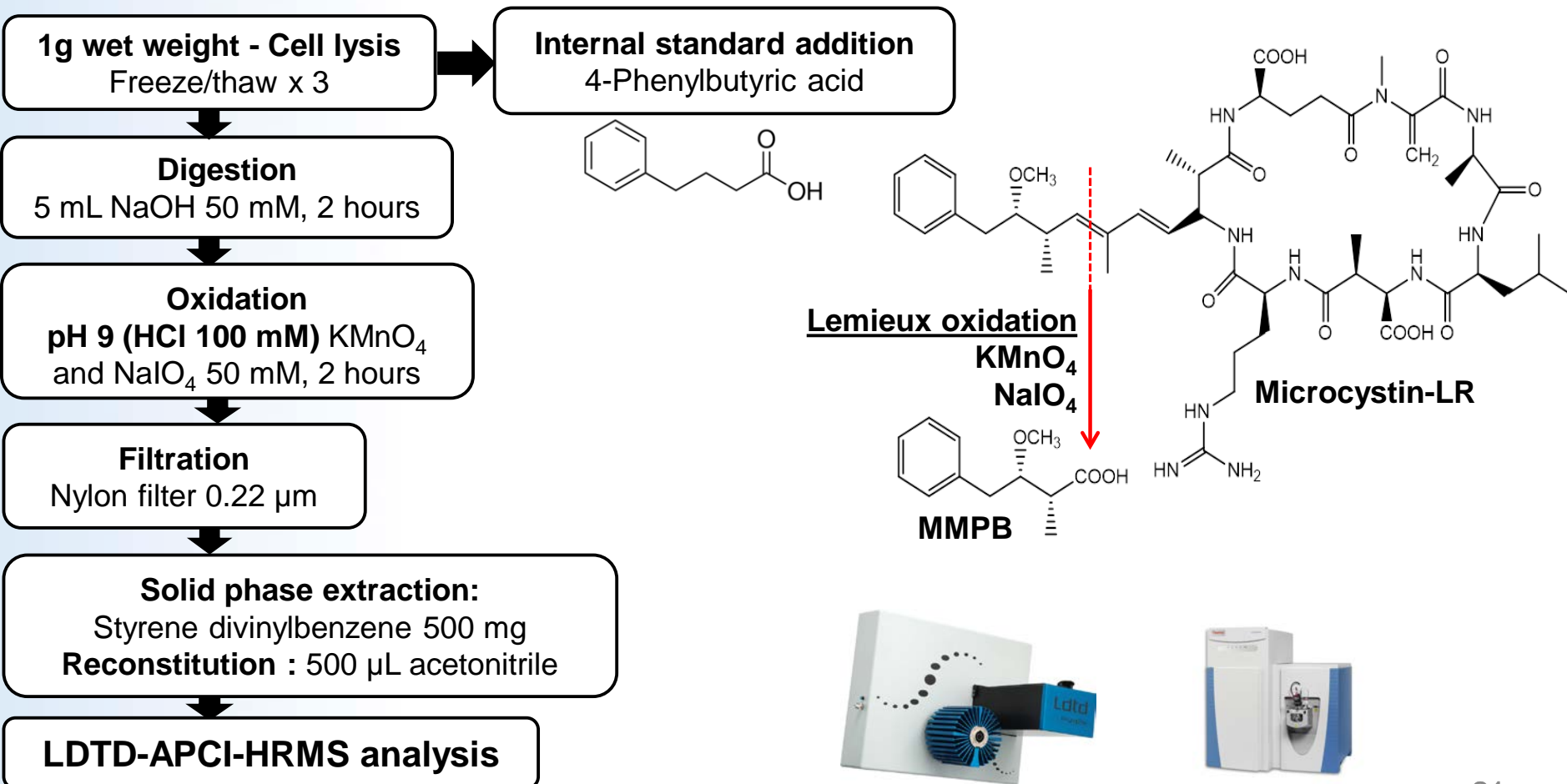
- More than **100 different microcystins** have been identified, but only a dozen certified standards are available.
- **Regulations in drinking and recreative waters:** 1  $\mu\text{g L}^{-1}$  (WHO)  
1.5  $\mu\text{g L}^{-1}$  (Canada).
- In aquatic environments, microcystins can **bioaccumulate**, microcystins may accumulate in food chains and thus be subjected to **biomagnification**.
- This bioaccumulation is due to the formation of irreversible links in the tissues of aquatic species, but is still **largely unknown**.



# Objectives

## Workflow

Lemieux oxidation to extract the MMPB moiety (2-methyl-3-methoxy-4 phenylbutyric acid), common to all microcystins congeners.





# Results for fish tissue

Comparison of total microcystins found in fish tissue samples using two analytical approaches.

Samples	Lakes	Fish species	Type of tissue	Total MCs via MMPB ( $\mu\text{g kg}^{-1}$ ) <sup>a</sup> (CV - %)	Total MCs with standards ( $\mu\text{g kg}^{-1}$ ) <sup>b</sup>
1	Lac Vert	Rainbow smelt	Viscera	11.9 (7)	ND
2	Lac Vert	White sucker	Whole	8.7 (8)	ND
3	Lac Vert	White sucker	Whole	13.2 (6)	2.0
4	Lac Vert	White sucker	Whole	9.5 (10)	ND
6	Lac Vert	Brook trout	Muscle	5.0 (10)	ND
7	Lac Vert	Brook trout	Muscle	4.5 (9)	ND
9	Lac Roxton	Yellow perch	Muscle	4.0 (10)	ND
11	Lac Roxton	Yellow perch	Muscle	3.1 (11)	ND
14	Lac Roxton	Yellow perch	Muscle	5.2 (9)	ND
17	Lac Noir	Yellow perch	Muscle	4.5 (7)	ND
18	Lac Noir	Yellow perch	Muscle	7.3 (11)	ND
20	Lac Noir	Yellow perch	Muscle	2.7 (12)	ND
22	Lac Noir	Walleye	Muscle	4.4 (8)	ND
24	Lac Noir	Walleye	Muscle	2.9 (10)	ND
27	Lac Noir	Walleye	Muscle	3.4 (9)	ND
33	Lac Noir	Brown bullhead	Muscle	3.8 (9)	ND
35	Lac Noir	Brown bullhead	Muscle	5.2 (8)	ND
38	Lac Noir	Lake whitefish	Muscle	7.1 (8)	ND
40	Lac Noir	Lake whitefish	Muscle	6.2 (9)	ND
41	Lac Noir	Lake whitefish	Muscle	5.9 (7)	ND
44	Lac Noir	Lake whitefish	Muscle	7.3 (10)	ND
45	Lac Noir	Lake whitefish	Muscle	4.5 (11)	ND
46	Lac Noir	Lake whitefish	Muscle	3.0 (9)	ND
49	Lac Noir	Yellow perch	Muscle	3.7 (11)	ND

**Digestion/oxidation: 70-75%**

**SPE recuperation : 91-98%**

**Matrix effects: 90-93%**

**LDM: 2.7  $\mu\text{g kg}^{-1}$**

**LQM: 8.2  $\mu\text{g kg}^{-1}$**

**Concentrations between 2.9 and 13.2  $\mu\text{g kg}^{-1}$**

<sup>a</sup>Total microcystins determined via MMPB using LDTD-APCI-HRMS.

<sup>b</sup>Microcystins determined via the summation of all microcystins for which standards allowed detection and quantification (i.e., MC-LA, MC-LR, MC-RR, and MC-YR) using LC-MS/MS.

# Results for water samples

82

A. Roy-Lachapelle et al. / *Analytica Chimica Acta* 820 (2014) 76–83**Table 3**

Comparison of total microcystins analysis of lakes samples using LDTD-APCI-MS/MS and LC-MS/MS.

No. Sample	Location	Date	Total MC via MMPB ( $\mu\text{g L}^{-1}$ ) <sup>a</sup> (RSD - %)	Total MC with standards ( $\mu\text{g L}^{-1}$ ) <sup>b</sup>	MC isomer without standards ( $\mu\text{g/L}$ ) <sup>c</sup>	Total MC ( $\mu\text{g L}^{-1}$ ) <sup>d</sup>	Percentage of MC with standards (%) <sup>e</sup>
1	Estrie	20130614	425 (9)	70	340 (RR) <sup>f</sup>	410	16
2	Estrie	20130614	1.0 (5)	0.15	0.5 (RR) <sup>f</sup>	0.65	15
3	Saguenay	20130620	5.4 (7)	1.6	3.3 (YR) <sup>f</sup>	4.9	30
4	Saguenay	20130620	4.7 (8)	1.8	2.5 (YR) <sup>f</sup>	4.3	38
5	Abitibi-Temiscamingue	20130624	ND	ND	ND	ND	–
6	Laurentides	20130731	37.4 (7)	35.4	ND	35.4	95
7	Abitibi-Temiscamingue	20130731	0.9 (8)	ND	ND	ND	–
8	Abitibi-Temiscamingue	20130731	2.7 (7)	0.59	ND	0.59	22
9	Monteregie	20130801	ND	0.1	ND	0.1	–

ND – Not detected.

<sup>a</sup> Total microcystins determined via MMPB using LDTD-APCI-MS/MS.<sup>b</sup> Microcystins determined via the summation of all microcystins for which standards allowed detection and quantification (i.e., HiLR, HtyR, LA, LF, LR, LR (D-Asp3), LW, LY, RR, RR (D-Asp3), WR, YR) using LC-MS/MS.<sup>c</sup> Microcystin isomer for which identification and concentration could not be certified due to the absence of appropriate standards using LC-MS/MS. Although their characteristics are slightly different from the available standard, there is a very high probability that these are isomers of LC-RR and LC-YR.<sup>d</sup> Total microcystins determined via the summation of all microcystins for which standards allowed detection and quantification and also for the suspected isomer tentatively identified using LC-MS/MS.<sup>e</sup> Percentage is calculated as: (MC isomer with standards/total MC via MMPB)  $\times$  100.<sup>f</sup> Suspected isomer of the specified congener.

# Determination of cyanotoxins in cyanobacterial dietary supplement samples

Cyanotoxins daily intake from CB dietary supplements samples ( $\mu\text{g}$ ) according to recommended maximum daily intake. Values in brackets represent the detected cyanotoxins as percentages of the WHO adult TDI guideline of  $0.04 \mu\text{g kg}^{-1}$  body weight for microcystins.

Samples	MCs tot	ANA-a	DH-ANA-a	E-ANA-a	CYN	STX	BMAA
<i>Spirulina</i>	ND	ND	ND	ND	ND	ND	ND
<i>Spirulina</i>	ND	ND	ND	ND	ND	ND	ND
<i>Spirulina</i>	ND	ND	ND	ND	ND	ND	ND
<i>Spirulina</i>	ND	ND	ND	ND	ND	ND	ND
<i>Spirulina</i>	ND	ND	ND	7.2	ND	ND	ND
<i>Spirulina</i>	ND	ND	ND	ND	ND	ND	ND
<i>Spirulina</i>	ND	ND	ND	ND	ND	ND	ND
<i>Spirulina</i>	0.25 (10)	ND	0.41	ND	ND	ND	ND
<i>Spirulina</i>	ND	ND	ND	ND	ND	ND	ND
<i>Spirulina</i>	ND	ND	ND	ND	ND	ND	ND
<i>Spirulina</i>	2.5 (104)	ND	ND	8.1	ND	ND	ND
<i>Spirulina</i>	ND	ND	ND	ND	ND	ND	ND
<i>Spirulina</i>	0.6 (25)	ND	ND	ND	ND	ND	ND
<i>Spirulina</i>	ND	ND	ND	ND	ND	ND	ND
<i>A. Flos-aquae</i>	16.4 (683)	ND	2.2	1.8	ND	ND	0.08
<i>A. Flos-aquae</i>	4.5 (188)	ND	ND	0.28	ND	ND	ND
<i>A. Flos-aquae</i>	3.3 (138)	0.35 (6)	5.8	ND	ND	ND	0.44
<i>A. Flos-aquae</i>	0.8 (33)	ND	ND	ND	ND	ND	ND

# Analytical automation

## Online SPE coupled to UHPLC and HRMS

- Sample extraction automated with the before chromatographic separation.
- Greater analytical capacity.
- Total MCs via MMPB: New method with LOD in water of 0.02  $\mu\text{g } \Sigma\text{MCs/L}$

### 14 cyanotoxins:

- Using 1 ml of sample with LC-HRMS in 7 min
- HRMS scans: allows to go back on the analyzes to identify known microcystins of which we do not have the standard.
- Inclusion of anatoxin-a transformation products.
- Same strategy for BMAA.

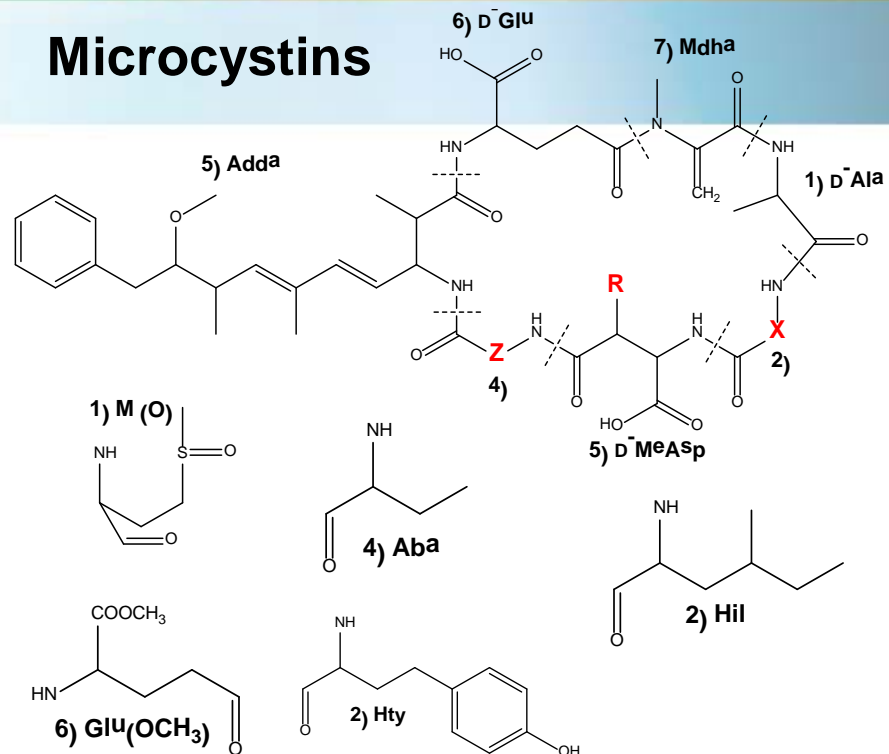
	MLD ( $\mu\text{g L}^{-1}$ )	MLQ ( $\mu\text{g L}^{-1}$ )
CYN	0.005	0.02
ANA-a	0.01	0.04
(DAsp <sup>3</sup> )MC-RR	0.009	0.03
MC-RR	0.007	0.02
MC-HtyR	0.02	0.05
MC-HiIR	0.009	0.05
MC-WR	0.01	0.04
MC-YR	0.01	0.04
MC-LR	0.01	0.04
(DAsp <sup>3</sup> )MC-LR	0.006	0.02
MC-LA	0.006	0.02
MC-LY	0.008	0.03
MC-LW	0.01	0.03
MC-LF	0.01	0.04



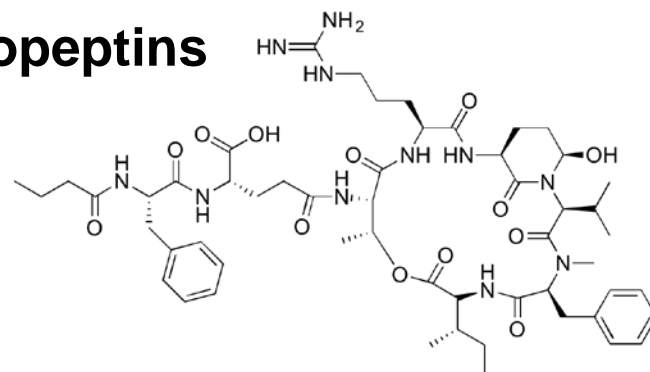
# Microcystins congeners

Microcystins	Molecular Formula	Exact Mass	X	Z	R	xLogP <sub>3</sub>	
MC-RR	[Asp <sup>3</sup> Dhb <sup>7</sup> ] MC-RR	C47H71N13O12	1009.53452	Arg	Arg	H	-0.7
	<b>[Asp<sup>3</sup>] MC-RR</b>	<b>C48H73N13O12</b>	<b>1023.55016</b>	<b>Arg</b>	<b>Arg</b>	<b>H</b>	<b>-0.4</b>
	<b>MC-RR</b>	<b>C49H75N13O12</b>	<b>1037.56582</b>	<b>Arg</b>	<b>Arg</b>	<b>CH<sub>3</sub></b>	<b>-0.2</b>
MC-YR	6(Z)-Adda MC-RR	C49H75N13O12	1037.56582	Arg	Arg	CH <sub>3</sub>	-0.2
	<b>MC-YR</b>	<b>C52H72N10O13</b>	<b>1044.52804</b>	<b>Tyr</b>	<b>Arg</b>	<b>CH<sub>3</sub></b>	<b>2.2</b>
	[Asp <sup>3</sup> Dhb <sup>7</sup> ] MC-LR	C47H70N10O12	966.51747	Leu	Arg	H	1.5
MC-LR	<b>[Asp<sup>3</sup>] MC-LR</b>	<b>C48H72N10O12</b>	<b>980.53312</b>	<b>Leu</b>	<b>Arg</b>	<b>H</b>	<b>2.1</b>
	<b>MC-LR</b>	<b>C49H74N10O12</b>	<b>994.54877</b>	<b>Leu</b>	<b>Arg</b>	<b>CH<sub>3</sub></b>	<b>2.3</b>
	6(Z)-Adda MC-LR	C49H74N10O12	994.54877	Leu	Arg	CH <sub>3</sub>	2.3
MC-XR	[Asp <sup>3</sup> ] MC-FR	C51H70N10O12	1014.51747	Phe	Arg	H	2.6
	MC-FR	C52H72N10O12	1028.53312	Phe	Arg	CH <sub>3</sub>	2.6
	[Asp <sup>3</sup> ] MC-WR	C53H71N11O12	1053.52837	Trp	Arg	H	2.7
MC-WR	<b>MC-WR</b>	<b>C54H73N11O12</b>	<b>1067.54402</b>	<b>Trp</b>	<b>Arg</b>	<b>CH<sub>3</sub></b>	<b>2.7</b>
	[Dhb <sup>7</sup> ] MC-HiR	C49H74N10O12	994.54877	HiI	Arg	H	2.3
	<b>MC-HiR</b>	<b>C50H76N10O12</b>	<b>1008.56442</b>	<b>HiI</b>	<b>Arg</b>	<b>CH<sub>3</sub></b>	<b>2.8</b>
MC-HtyR	[Dhb <sup>7</sup> ] MC-HtyR	C52H72N10O13	1044.52803	Hty	Arg	H	2.6
	<b>MC-HtyR</b>	<b>C53H74N10O13</b>	<b>1072.55934</b>	<b>Hty</b>	<b>Arg</b>	<b>CH<sub>3</sub></b>	
	[Asp <sup>3</sup> ] MC-RA	C45H66N10O12	938.48617	Arg	Ala	H	
MC-RA	MC-RA	C46H68N10O12	952.50182	Arg	Ala	CH <sub>3</sub>	1?
	[Asp <sup>3</sup> ] MC-Raba	C46H68N10O12	952.50182	Arg	Aba	H	
	MC-Raba	C47H70N10O12	966.51747	Arg	Aba	CH <sub>3</sub>	
MC-RL	MC-RL	C49H74N10O12	994.54877	Arg	Leu	CH <sub>3</sub>	
	MC-YA	C49H66N7O13	959.46404	Tyr	Ala	CH <sub>3</sub>	3.4
	[Asp <sup>3</sup> ] MC-LA	C45H65N7O12	895.46912	Leu	Ala	H	
MC-LA	<b>MC-LA</b>	<b>C46H67N7O12</b>	<b>909.48477</b>	<b>Leu</b>	<b>Ala</b>	<b>CH<sub>3</sub></b>	<b>3.5</b>
	[Asp <sup>3</sup> ] MC-LAba	C46H67N7O12	909.48477	Leu	Aba	H	
	MC-LAba	C47H69N7O12	925.50042	Leu	Aba	CH <sub>3</sub>	3.7
MC-XA	[Asp <sup>3</sup> ] MC-FA	C48H63N7O12	929.45347	Phe	Ala	H	
	MC-FA	C49H65N7O12	943.46912	Phe	Ala	CH <sub>3</sub>	3.4
	MC-FAba	C50H67N7O12	957.48477	Phe	Aba	CH <sub>3</sub>	
MC-WA	[Asp <sup>3</sup> ] MC-WA	C50H64N8O12	968.46437	Trp	Ala	H	
	MC-WA	C51H66N8O12	982.48002	Trp	Ala	CH <sub>3</sub>	3.5
	MC-WAba	C52H68N8O12	996.49567	Trp	Aba	CH <sub>3</sub>	
MC-LL	MC-LL	C49H73N7O12	951.53172	Leu	Leu	CH <sub>3</sub>	4.8
	MC-FL	C52H71N7O12	985.51607	Phe	Leu	CH <sub>3</sub>	
	MC-WL	C54H72N8O12	1024.52697	Trp	Leu	CH <sub>3</sub>	4
MC-LY	<b>MC-LY</b>	<b>C52H71N7O13</b>	<b>1001.51099</b>	<b>Leu</b>	<b>Tyr</b>	<b>CH<sub>3</sub></b>	<b>4.7</b>
	<b>MC-LW</b>	<b>C54H72N8O12</b>	<b>1024.52697</b>	<b>Leu</b>	<b>Trp</b>	<b>CH<sub>3</sub></b>	<b>5.2</b>
	<b>MC-LF</b>	<b>C52H71N7O12</b>	<b>985.51607</b>	<b>Leu</b>	<b>Phe</b>	<b>CH<sub>3</sub></b>	<b>5.1</b>
MC-AW	MC-AW	C51H66N8O12	982.48002	Ala	Trp	CH <sub>3</sub>	3.9
	MC-YM	C51H69N7O13S	1019.46741	Tyr	Met	CH <sub>3</sub>	4.1
	MC-VF	C51H69N7O12	971.50042	Val	Phe	CH <sub>3</sub>	4.7

## Microcystins



## Micropeptins



Micropeptin 1106, Exact Mass 1105.5808

# Acknowledgment

Prof. Sébastien Sauvé

Morgan Solliec

Sung Vo Duy

Paul B. Fayad

Marc Sinotte

and Christian Deblois - Développement durable, Environnement et Lutte contre les changements climatiques (MDDELCC)

Phytronix Technologies team

Unity Lab Services - Thermo Scientific team



**And thank you for your attention!**



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